and second oligonucleotides each independently comprising at least 15 contiguous nucleotides chosen from any of SEQ ID NOs: 1, 2, 3, 4, 20 and 27, or the complement thereof wherein W represents A or T, R represents G or A and Y represents T or C, or a corresponding sequence wherein T has been replaced by U.

- 39. (new) A polynucleic acid consisting of 10 to 50 nucleotides which specifically hybridizes under conditions allowing discrimination of up to 1 nucleotide mismatch with the sequence of SEQ ID NO:20 wherein Y represents T or C, or with a corresponding sequence wherein T has been replaced by U.
- 40. (new) A polynucleic acid consisting of 21 to 50 nucleotides which specifically hybridizes with the sequence of SEQ ID NO:20 or the complement thereof wherein Y represents T or C, or with a corresponding sequence wherein T has been replaced by U.
- 41. (new) A polynucleic acid consisting of 21 to 50 nucleotides which specifically hybridizes under conditions allowing discrimination of up to 1 nucleotide mismatch with the sequence of SEQ ID NO:20 or the complement thereof wherein Y represents T or C, or with a corresponding sequence wherein T has been replaced by U.
  - 42. (new) A polynucleic acid consisting of 27 to 50 nucleotides which specifically

hybridizes under conditions allowing discrimination of up to 1 nucleotide mismatch with the sequence of SEQ ID NO:27 or the complement thereof, or with a corresponding sequence wherein T has been replaced by U.

- 43. (new) A method for detecting the presence of an infection with an HCV virus in a biological sample by means of a hybridization reaction with a set of oligonucleotides of claims 25 or 38.
- 44. (new) A method according to claim 43 wherein said oligonucleotides are coupled to a solid support.
- 45. (new) A method according to claim 28 wherein said polynucleic acids are capture probes.
- 46. (new) A method according to claim 29 wherein said polynucleic acids are capture probes.
- 47. (new) A method according to claim 43 wherein said oligonucleotides are capture probes.
  - 48. (new) A method for detecting the presence of an infection with an HCV virus

in a biological sample by means of an amplification reaction using (a set of) primers that specifically hybridize with SEQ ID NO: 1 or SEQ ID NO:3, or the complement thereof wherein W represents A or T, R represents G or A and Y represents T or C; and with SEQ ID NO:20 or SEQ ID NO:27, or the complement thereof wherein Y represents T or C.

- 49. (new) A method for detecting the presence of an infection with an HCV virus in a biological sample by means of an amplification reaction using (a set of) primers that specifically hybridize with SEQ ID NO:20 or SEQ ID NO:27, or the complement thereof wherein Y represents T or C; and with SEQ ID NO:2 or SEQ ID NO:4, or the complement thereof.
- 50. (new) A diagnostic kit for the detection of HCV in a biological sample comprising a set of oligonucleotides of claims 25 or 38.
- 51. (new) A method for the identification of a previously amplified HCV 5' untranslated region fragment comprising hybridizing a set of oligonucleotides of claims 25 or 38 to said 5' region.
- 52. (new) The process of claim 36 wherein said primer of 15 to 50 nucleotides specifically hybridizing with SEQ ID NO: 1 is combined with a primer hybridizing to the

region extending from nucleotide -68 to nucleotide -1 or the complement of said region.

53. (new) The process of claim 36 wherein said primer of 15 to 50 nucleotides specifically hybridizing with SEQ ID NO:3 is combined with a primer hybridizing to the region extending from nucleotide -68 to nucleotide -1 or the complement of said region.

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54. (new) The process according to claim 52 or 53 wherein said primer hybridizing to the region extending from nucleotide -68 to nucleotide -1 or the complement of said region is defined by SEQ ID NO:2 or SEQ ID NO:4.--

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